

Genetic profile for Little White Salmon NFH

Spring Chinook salmon

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National Fish Hatchery Broodstock Genetic Profile

Facility: Little White Salmon National Fish Hatchery

Stock: Spring Chinook salmon (*Oncorhynchus tshawytscha*)

Parental stock: Hatchery-origin spring Chinook salmon from Carson NFH and Rapid River Fish Hatchery

Year founded: Local returns of unknown origin breed in 1967, considered a derivative of “Carson” stock

Generation time: 3-5 years (y) (3% 3y, 86% 4y, 11% 5y)

Segregation/Integration history: Segregated. Only hatchery-origin fish trapped at Little White Salmon NFH are used for broodstock.

Table 1- Broodstock samples analyzed:

Description	Year	n	Life stage	Data source	Code
Little White Salmon NFH	2007	93	Juvenile	FishGen	LWS2007
Little White Salmon NFH	2013	625	Returning adult	CRITFC	LWS2013
Little White Salmon NFH	2014	759	Returning adult	CRITFC	LWS2014

Table 2 - Samples analyzed for comparison:

Description	Year	n	Life stage	Data source	Code
Carson NFH	2012	933	Returning adult	CRITFC	CARS2012
Carson NFH	2013	911	Returning adult	CRITFC	CARS2013
Carson NFH	2014	949	Returning adult	CRITFC	CARS2014
John Day River wild	2000	9	Juvenile	FishGen	JDAY2000
John Day River wild	2004	69	Returning adult	FishGen	JDAY2004
John Day River wild	2006	89	Returning adult	FishGen	JDAY2006
Klickitat SFH	2002	45	Returning adult	FishGen	KLICK2002
Klickitat SFH	2006	40	Returning adult	FishGen	KLICK2006
Klickitat SFH	2012	251	Returning adult	CRITFC	KLICK2012
Klickitat SFH	2013	372	Returning adult	CRITFC	KLICK2013
Klickitat SFH	2014	408	Returning adult	CRITFC	KLICK2014
Parkdale Fish Facility	2012	130	Returning adult	CRITFC	PFF2012
Parkdale Fish Facility	2013	48	Returning adult	CRITFC	PFF2013
Parkdale Fish Facility	2014	221	Returning adult	CRITFC	PFF2014
Shitike Creek wild	2004	93	Juvenile	FishGen	WSHCR2004
Warm Springs NFH	2004	89	Returning adult	FishGen	WSNFH2004
Warm Springs NFH	2012	439	Returning adult	CRITFC	WSNFH2012
Warm Springs NFH	2013	494	Returning adult	CRITFC	WSNFH2013
Warm Springs NFH	2014	100	Returning adult	CRITFC	WSNFH2014

Genetic markers analyzed:

186 single nucleotide polymorphism (SNP) markers (Appendix 1).

Table 3: Diversity within samples

Expected (H_E) and observed (H_O) heterozygosity, number of loci exhibiting departures from Hardy-Weinberg Proportions (HWP), and F_{IS} (a measure of departure from random mating). Values of F_{IS} in bold were bounded by a 95% confidence interval that did not overlap zero.

Population	H_O	H_E	F_{IS}	HWE
LWS2007	0.24	0.24	0.0089	14
LWS2013	0.24	0.24	-2.00E-04	12
LWS2014	0.24	0.24	-0.0056	20
CARS2012	0.24	0.24	0.0079	23
CARS2013	0.24	0.24	0.0076	18
CARS2014	0.24	0.24	-0.0054	11
JDAY2000	0.23	0.21	-0.0611	3
JDAY2004	0.24	0.25	0.0123	9
JDAY2006	0.24	0.24	-0.0069	3
KLICK2002	0.29	0.29	-0.017	5
KLICK2006	0.31	0.3	-0.029	6
KLICK2012	0.31	0.31	-0.0013	12
KLICK2013	0.31	0.3	-0.0021	13
KLICK2014	0.3	0.3	5.00E-04	21
PFF2012	0.25	0.26	0.0178	28
PFF2013	0.23	0.23	0.018	9
PFF2014	0.25	0.25	0.0162	31
WSHCR2004	0.23	0.23	-0.0171	6
WSNFH2004	0.25	0.24	-0.0255	11
WSNFH2012	0.24	0.24	0.008	22
WSNFH2013	0.25	0.24	-0.0029	27
WSNFH2014	0.25	0.25	-0.0264	11

Figure 1: Correspondence Analysis (CA) of allele frequencies observed in spring Chinook salmon from Little White Salmon NFH and adjacent collection sites.

The primary (horizontal) axis accounted for 41.2% of the inertia in the data and the secondary (vertical) axis accounted for 27% of the inertia. Label match the population codes used in Table 2.

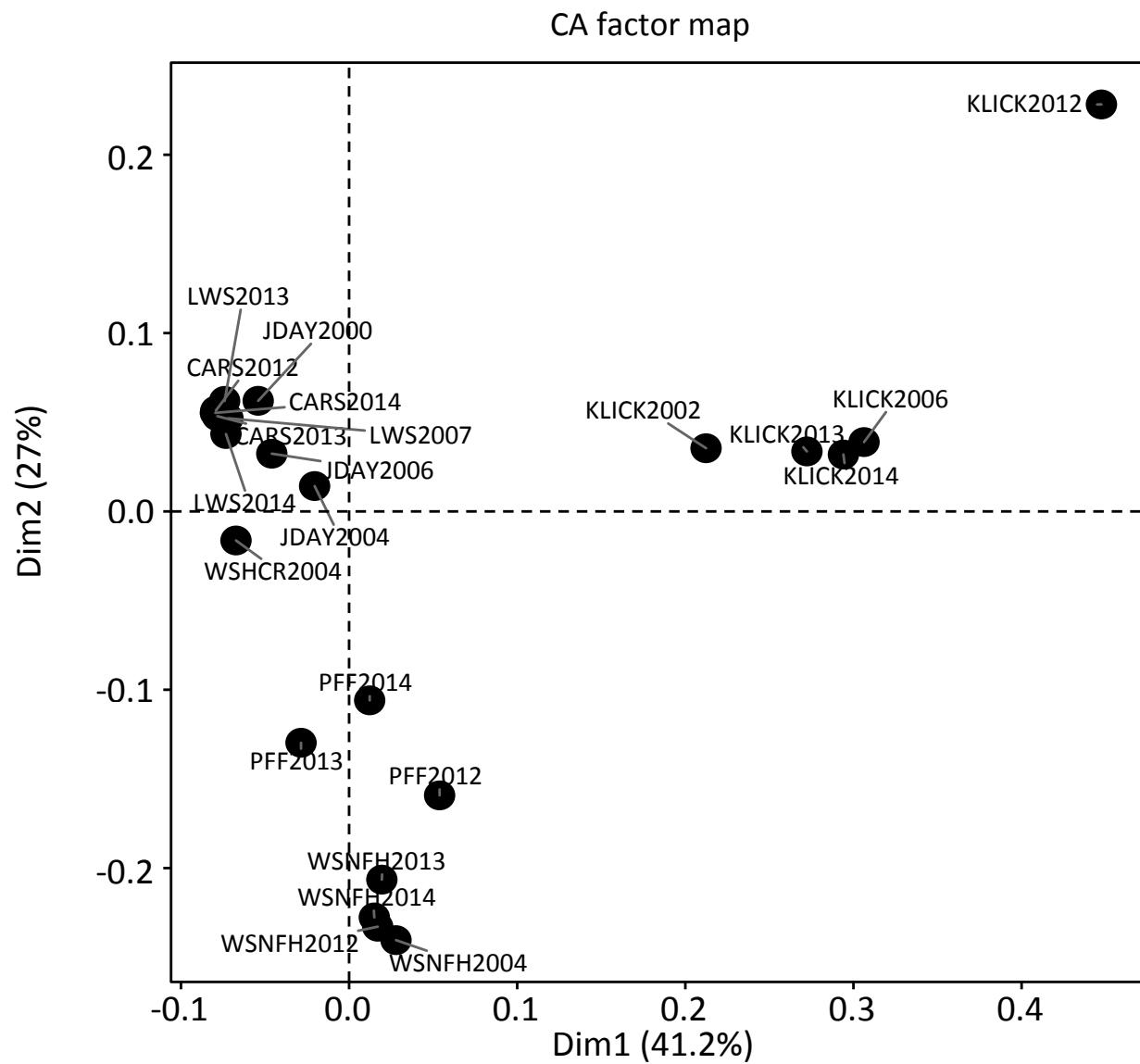


Figure 2: Estimates of effective population size (N_E) for spring Chinook salmon broodstock from Little White Salmon NFH and adjacent collection sites.

N_E was estimated using the linkage-disequilibrium method. Each point estimate is surrounded by a jackknifed 95% confidence interval.

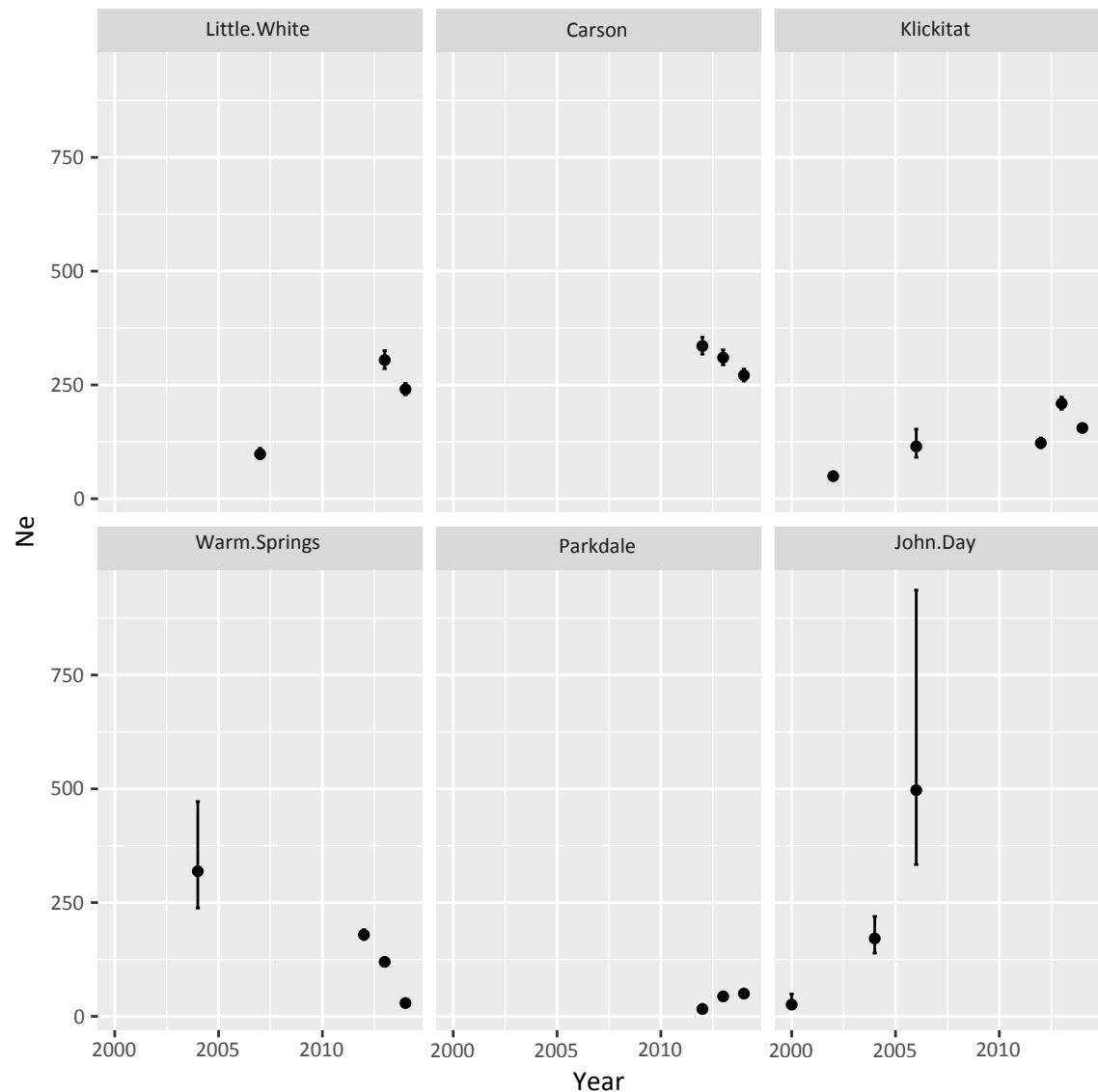
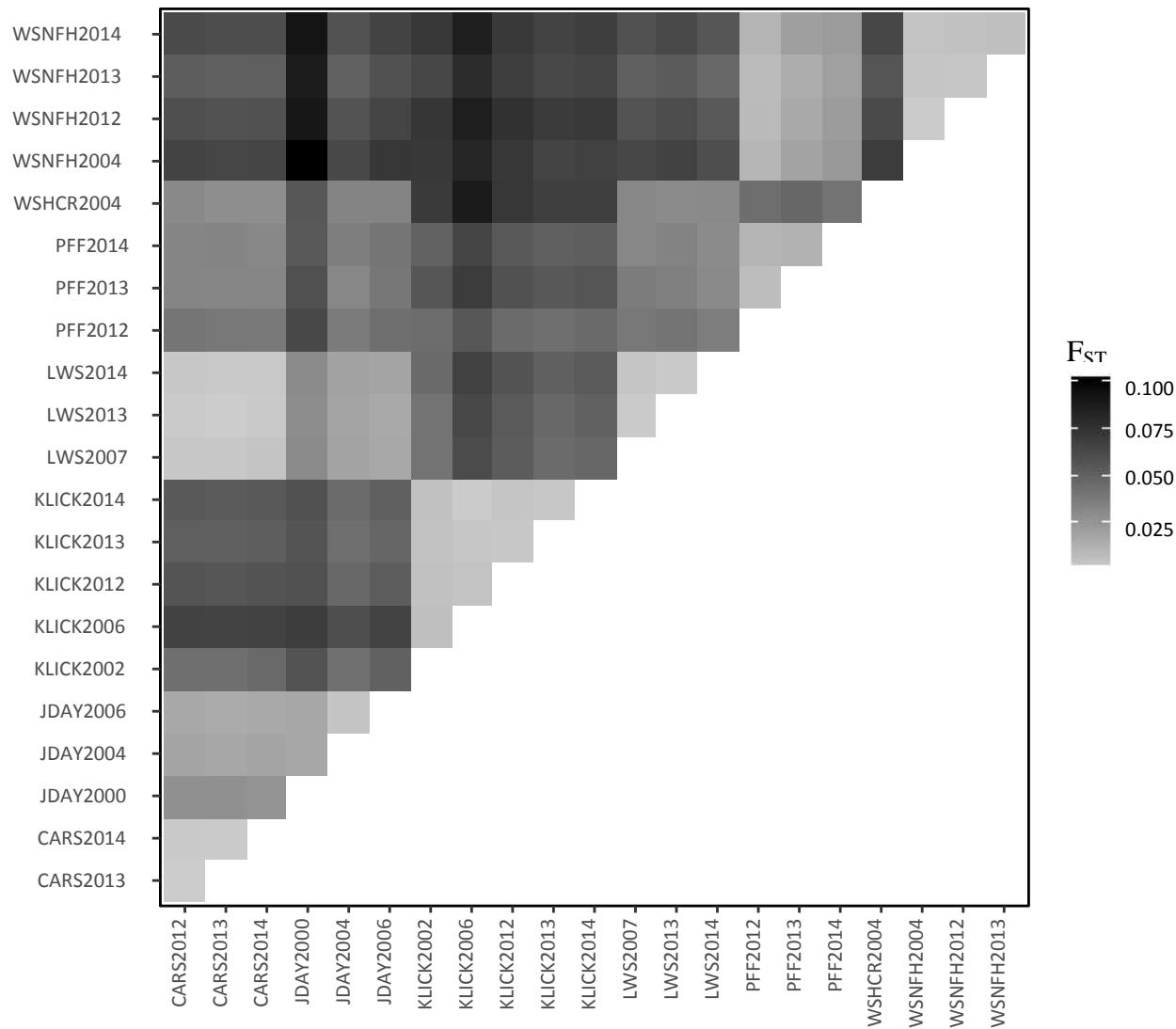


Figure 3: Heatmap of pairwise F_{ST} values between for spring Chinook broodstock from Little White Salmon NFH and adjacent collection sites.



Comments

- The goals of this report series is to 1) summarize available genetic information for NFH broodstocks and make that information available to hatchery managers, and 2) make sure that data for the NFH broodstocks are available for internal hatchery reviews and HET meetings, as well as to our partners.
- Genetic diversity (heterozygosity) was nearly equal across the broodstocks that were analyzed, except for the Klickitat State Hatchery that had the highest levels of heterozygosity. Little White Salmon NFH broodstock were comparable to other groups that were sampled and consistent across years.
- For the number of loci analyzed for this report (186), the amount deviating from HWP was moderate for these broodstocks (between 2-17%). Little White Salmon broodstock had between 7-11% of loci deviating from HWP depending on the year. Values of F_{IS} were low and only five broodstocks displayed values that statistically deviated from zero. This suggests that forces such as inbreeding and genetic drift are not significantly impacting the genetics of the broodstock.
- The correspondence analysis revealed that Little White Salmon NFH broodstock were indistinguishable from each other and clustered closely with Carson NFH broodstock. Surprisingly, wild populations from the John Day watershed were the next closest in the plot. Broodstocks from the same hatchery tended to cluster more closely together than to other groups.
- The majority of pairwise F_{ST} comparisons were statistically significant, meaning the observed values were greater than expected if there was no differentiation. The patterns of differentiation mirrored those of the correspondence analysis. Little White Salmon NFH broodstocks were weakly differentiated from each other; they were also weakly differentiated from Carson NFH broodstocks.
- Estimates of effective population size were variable, even within individual hatcheries across years. The first year of data for Little White Salmon NFH was from 2007 and produced the lowest N_E estimate (98.1) for that hatchery. Estimates from 2013 and 2014 (304.7 and 240.5, respectively) were much higher.

Availability

Genotype data for NFH stocks are available from the FishGen database (www.fishgen.net) and the Columbia River Inter-Tribal Fish Commission, and will be provided by AFTC upon request.

Disclaimer

The findings and conclusions in this report are those of the author and do not necessarily represent the views of the U.S. Fish and Wildlife Service.

Appendix 1: 186 single nucleotide polymorphism (SNP) markers used to analyze Little White Salmon NFH spring Chinook salmon.

Single nucleotide polymorphisms				
Ots_100884-287	Ots_hsc71-5'-453	Ots_Prl2	Ots_U2446-123	Ots_117432-409
Ots_102867-609	Ots_hsp27b-150	Ots_RAG3	Ots_u4-92	Ots_118175-479
Ots_brp16-64	Ots_Hsp90a	Ots_RAS1	Ots_u6-75	Ots_118205-61
Ots_Cath_D141	Ots_HSP90B-100	Ots_redd1-187	Ots_unk1104-38	Ots_102213-210
Ots_CCR7	Ots_101119-381	Ots RFC2-558	Ots_unk1832-39	Ots_118938-325
Ots_CD59-2	Ots_IGF-I.1-76	Ots_S7-1	Ots_unk3513-49	Ots_122414-56
Ots_CD63	Ots_Ikaros-250	Ots_SClkF2R2-135	Ots_unk526	Ots_123048-521
Ots_CirpA	Ots_IL11	Ots_106499-70	Ots_unk7936-50	Ots_123921-111
Ots_cox1-241	Ots_IL8R_C8	Ots_SL	Ots_unk9480-51	Ots_124774-477
Ots_CRB211	Ots_LWSop-638	Ots_stk6-516	Ots_101554-407	Ots_127236-62
Ots_103122-180	Ots_mapK-3'-309	Ots_SWS1op-182	Ots_107806-821	Ots_128302-57
Ots_104415-88	Ots_105407-117	Ots_TAPBP	Ots_vatf-251	Ots_102414-395
Ots_105105-613	Ots_mapKpr-151	Ots_TCTA-58	Ots_zn593-346	Ots_128693-461
Ots_DDX5-171	Ots_MHC1	Ots_TGFB	Ots_zP3b-215	Ots_128757-61R
Ots_E2-275	Ots_MHC2	Ots_Thio	Ots_ZR-575	Ots_129144-472
Ots_EndoRB1-486	Ots_mybp-85	Ots_TLR3	Ots_108007-208	Ots_129458-451
Ots_EP-529	Ots_Myc-366	Ots_TNF	Ots_108390-329	Ots_130720-99
Ots_Est1363	Ots_myo1a-384	Ots_106747-239	Ots_108735-302	Ots_131460-584
Ots_Est740	Ots_myoD-364	Ots_Tnsf	Ots_108820-336	Ots_131906-141
Ots_ETIF1A	Ots_nelfd-163	Ots_tpx2-125	Ots_109525-816	Ots_102457-132
Ots_105132-200	Ots_NFYB-147	Ots_txnip-321	Ots_109693-392	Ots_94857-232R
Ots_FARSLA-220	Ots_nkef-192	Ots_u07-07.161	Ots_110064-383	Ots_94903-99R
Ots_FGF6A	Ots_NOD1	Ots_u07-17.135	Ots_110201-363	Ots_96222-525
Ots_FGF6B_1	Ots_nramp-321	Ots_u07-18.378	Ots_101704-143	Ots_96500-180
Ots_GCSH	Ots_ntl-255	Ots_u07-20.332	Ots_110495-380	Ots_96899-357R
Ots_GDH-81x	Ots_OTALDBINT1- -SNP1	Ots_107074-284	Ots_110551-64	Ots_97077-179R
Ots_GH2	Ots_OTDESMIN19- -SNP1	Ots_u07-25.325	Ots_110689-218	Ots_102801-308
Ots_GnRH-271	Ots_Ots311-101x	Ots_u07-49.290	Ots_111681-657	Ots_99550-204
Ots_GPDH-338	Ots OTSMTA- -SNP1	Ots_u07-53.133	Ots_112208-722	Ots_AldB1-122
Ots_GPH-318	Ots_OTSTF1-SNP1	Ots_u07-57.120	Ots_112301-43	Ots_aldb-177M
Ots_GST-207	Ots_P450	Ots_u07-64.221	Ots_112419-131	Ots_ARNT
Ots_105385-421	Ots_P450-288	Ots_u1002-75	Ots_112820-284	Ots_arp-436
Ots_GST-375	Ots_P53	Ots_u1007-124	Ots_112876-371	Ots_AsnRS-60
Ots_GTH2B-550	Ots_parp3-286	Ots_107285-93	Ots_113242-216	Ots_aspat-196
Ots_HFABP-34	Ots_PGK-54	Ots_u202-161	Ots_113457-40R	
Ots_HMGB1-73	Ots_pigh-105	Ots_u211-85	Ots_115987-325	
Ots_hnRNPL-533	Ots_pop5-96	Ots_U2362-227	Ots_117242-136	
Ots_hsc71-3'-488	Ots_ppie-245	Ots_U2362-330	Ots_117259-271	

Appendix 2: Pairwise F_{ST} values between spring Chinook salmon broodstock produced at Little White Salmon NFH and adjacent collection sites.

Sample numbers are those listed in Table 3. The 95% confidence interval for all estimates did not overlap zero.

	LWS2007	LWS2013	LWS2014
LWS2007	*		
LWS2013	0.0022	*	
LWS2014	0.0043	0.0028	*
CARS2012	0.0035	0.0022	0.0037
CARS2013	0.0037	0.0014	0.0031
CARS2014	0.0051	0.0029	0.003
JDAY2000	0.0305	0.0299	0.0306
JDAY2004	0.0197	0.0193	0.0199
JDAY2006	0.0174	0.0169	0.0191
KLICK2002	0.0422	0.0423	0.0467
KLICK2006	0.0624	0.064	0.0676
KLICK2012	0.0537	0.0547	0.0582
KLICK2013	0.0461	0.0476	0.0515
KLICK2014	0.0482	0.0512	0.0545
PFF2012	0.0395	0.0417	0.0375
PFF2013	0.0378	0.0359	0.0314
PFF2014	0.0327	0.0345	0.0309
WSHCR2004	0.0328	0.0308	0.0313
WSNFH2004	0.0642	0.0671	0.0606
WSNFH2012	0.0579	0.0614	0.0551
WSNFH2013	0.0513	0.0538	0.0476
WSNFH2014	0.059	0.0634	0.0563

Appendix 3: Glossary

Allele – A unique genetic character state. Each locus has two alleles.

Effective population size (N_E) – The number of individuals in a model population which would lose genetic variation at the same rate as an observed population. Deviations from model behavior in real populations (e.g. unequal sex ratios, some individuals reproducing more than others, etc...) tend to make N_E lower than census size (N).

F_{IS} – Correlation of alleles in an individual relative to the subpopulation in which it occurs. Commonly used as a measure of departure from random mating within a subpopulation.

F_{ST} – Correlation of alleles within the same subpopulation relative to the entire population. Commonly used as a measure of divergence between subpopulations.

Gene flow – Movement of genetic material from one population to another. Implies both physical movement and successful integration into the recipient population.

Genetic Drift – Process of genetic divergence between populations based on random sampling of alleles each generation.

Heterozygosity – Proportion of individuals in a population that are heterozygotes (i.e. do not have two identical alleles at a locus).

Hardy-Weinberg Proportions (HWP) – Genotype ratios expected under a random mating model.

Locus – A physical location on the DNA of an organism. The term “locus” is often used synonymously with “marker” or with any type of marker (e.g., “SNP” or “microsatellite”).